```
                    GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:   November 29, 2004, 07:44:37 ; Search time 153 Seconds
                                         (without alignments)
                             11.723 Million cell updates/sec

Title:         HOLLY-9
Perfect score: 22
Sequence:      1 aaaag 5

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters:   2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   A_Geneseq_23sep04:*
     1: geneseqp1980s:*
     2: geneseqp1990s:*
     3: geneseqp2000s:*
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     5: geneseqp2002s:*
     6: geneseqp2003as:*
     7: geneseqp2003bs:*
     8: geneseqp2004s:*
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[handwritten annotations]

Pred. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	Match Length	DB	ID	Description
1	22	100.0	22	6	2	AAY42597	Aay42597 Human IgE
2	22	100.0	22	6	2	AAY85229	Aay85229 Human IgE
3	22	100.0	22	6	4	AAB82095	Aab82095 Hamster P
4	22	100.0	22	6	5	AAE15586	Aae15586 Hamster P
5	22	100.0	22	7	4	AAY69877	Aay69877 13C-label
6	22	100.0	22	7	4	AAB73728	Aab73728 Radiolabe
7	22	100.0	22	7	6	ADA38160	Ada38160 Peptide c
8	22	100.0	22	8	4	AAW83379	Aaw83379 Beta-amyl
9	22	100.0	22	8	4	AAB82093	Aab82093 Hamster P
10	22	100.0	22	8	5	ABG71017	Abg71017 Prion pro
11	22	100.0	22	8	5	ABB05165	Abb05165 Prion pro
12	22	100.0	22	8	5	AAE15584	Aae15584 Hamster P
13	22	100.0	22	8	7	AAE26268	Aae26268 Human amy
14	22	100.0	22	8	7	ADD24684	Add24684 Peptide a
15	22	100.0	22	9	5	ADJ64068	Adj64068 Human bet
16	22	100.0	22	10	4	AAW43905	Aaw43905 Specific
17	22	100.0	22	10	4	ABG65845	Abg65845 Peptide 1
18	22	100.0	22	10	4	AAG84197	Aag84197 Arabidops
19	22	100.0	22	10	4	AAG84188	Aag84188 Arabidops
20	22	100.0	22	10	4	AAG97948	Aag97948 Human com
21	22	100.0	22	10	4	AAG97712	Aag97712 Human com
22	22	100.0	22	10	4	AAG97945	Aag97945 Human com
23	22	100.0	22	10	4	AAG97947	Aag97947 Human com
24	22	100.0	22	10	4	AAG97946	Aag97946 Human com
25	22	100.0	22	10	5	ABG65858	Abg65858 Peptide 1
26	22	100.0	22	10	5	ABG65874	Abg65874 Peptide 1
27	22	100.0	22	11	6	ADA38149	Ada38149 Peptide a
28	22	100.0	22	11	6	ADA38151	Ada38151 Control p
29	22	100.0	22	11	6	AAO31161	Aao31161 Prion (Pr
30	22	100.0	22	11	6	AAO31163	Aao31163 Prion (Pr
31	22	100.0	22	11	7	ADC23466	Adc23466 Peptide a
32	22	100.0	22	11	7	ADC23468	Adc23468 Peptide a
33	22	100.0	22	11	7	ADD24690	Add24690 Peptide a
34	22	100.0	22	11	7	ADD24689	Add24689 Peptide a
35	22	100.0	22	12	2	AAW22038	Aaw22038 Antigenic
36	22	100.0	22	12	4	AAW32561	Aaw32561 Prion tar
37	22	100.0	22	12	4	AAB37466	Aab37466 ATP-depen
38	22	100.0	22	12	6	ABG71386	Abg71386 Staphyloc
39	22	100.0	22	12	6	ABU79022	Abu79022 Prion pro
40	22	100.0	22	12	6	ABW00156	Abw00156 Anti-PrP
41	22	100.0	22	12	7	ADE29207	Ade29207 Multivale
42	22	100.0	22	12	8	ADH80963	Adh80963 Peptide r
43	22	100.0	22	12	8	ADH80962	Adh80962 Peptide r
44	22	100.0	22	12	8	ADL70328	Adl70328 Peptide a
45	22	100.0	22	12	8	ADL70310	Adl70310 Peptide a
46	22	100.0	22	12	8	ADL70316	Adl70316 Peptide a
47	22	100.0	22	12	8	ADL70325	Adl70325 Peptide a
48	22	100.0	22	12	8	ADL70313	Adl70313 Peptide a
49	22	100.0	22	12	8	ADL70319	Adl70319 Peptide a
50	22	100.0	22	12	8	ADL70322	Adl70322 Peptide a
51	22	100.0	22	12	8	ADN37740	Adn37740 Hard segm
52	22	100.0	22	13	5	AAY67844	Aay67844 Alpha-2 a
53	22	100.0	22	13	5	ADG66555	Adg66555 B. subtil
54	22	100.0	22	13	5	ADG66553	Adg66553 B. subtil
55	22	100.0	22	13	5	ADG66552	Adg66552 B. subtil
56	22	100.0	22	13	5	ADG66556	Adg66556 B. subtil
57	22	100.0	22	13	5	ADG66554	Adg66554 B. subtil
58	22	100.0	22	13	6	AAO31195	Aao31195 Human bet
59	22	100.0	22	13	7	ADC23477	Adc23477 Peptide a
60	22	100.0	22	13	7	ADC23476	Adc23476 Peptide a
61	22	100.0	22	14	7	AAW17679	Aaw17679 Prion pro
62	22	100.0	22	14	2	AAW17680	Aaw17680 Prion pro
63	22	100.0	22	14	2	AAW69817	Aaw69817 Peptide f
64	22	100.0	22	14	2	AAW73743	Aaw73743 M. tuberc
65	22	100.0	22	14	2	AAW73853	Aaw73853 M. tuberc
66	22	100.0	22	14	4	AAU08208	Aau08208 Mycobacte
67	22	100.0	22	14	4	ABU79033	Abu79033 Prion pro
68	22	100.0	22	14	6	ABP74859	Abp74859 Proteome
69	22	100.0	22	14	6	ABP58083	Abp58083 Human pri
70	22	100.0	22	14	5	ABW00167	Abw00167 Prion (Pr
71	22	100.0	22	15	5	ABB09749	Abb09749 Peptide f
72	22	100.0	22	16	2	AAR04447	Aar04447 Human imm
73	22	100.0	22	16	2	AAR04483	Aar04483 Human imm
74	22	100.0	22	16	4	ABU54074	Abu54074 Human DNA
75	22	100.0	22	16	7	ADL34426	Adl34426 MHC/HLA p
76	22	100.0	22	17	7	AAM78078	Aam78078 Human bon
77	22	100.0	22	17	5	ABG47084	Abg47084 Human pep
78	22	100.0	22	17	8	ABO54338	Abo54338 Human gen
79	22	100.0	22	18	8	AAR07530	Aar07530 B-cell ep
80	22	100.0	22	18	6	AAW23360	Aaw23360 Human bet
81	22	100.0	22	18	2	AAW67021	Aaw67021 Peptide M
82	22	100.0	22	18	2	AAW81054	Aaw81054 Signal pe
83	22	100.0	22	18	3	AAB23279	Aab23279 Momordica
84	22	100.0	22	18	8	ADA66316	Ada66316 M. charan
85	22	100.0	22	18	8	ADO08751	Ado08751 Novel sur
86	22	100.0	22	19	2	AAR36792	Aar36792 Prion pro
87	22	100.0	22	19	2	AAR36794	Aar36794 Prion pro
88	22	100.0	22	19	6	AAW17681	Aaw17681 Prion pro
89	22	100.0	22	19	6	ABP58082	Abp58082 Human pri
90	22	100.0	22	19	6	ABU62604	Abu62604 Hypotheti
91	22	100.0	22	19	6	ABO58531	Abo58531 Human gen
92	22	100.0	22	20	2	AAR07528	Aar07528 B-cell ep
93	22	100.0	22	20	3	AAW32319	Aaw32319 Leishmani
94	22	100.0	22	20	3	AAB03085	Aab03085 N-terminu
95	22	100.0	22	20	4	AAB69493	Aab69493 Synthetic
96	22	100.0	22	20	4	AAB73061	Aab73061 Machado-J
97	22	100.0	22	20	4	AAE12262	Aae12262 Mycobacte
98	22	100.0	22	20	5	AAE13243	Aae13243 Human pep

No.	Len	%ID	Sc	Ct	Accession	Description
99	22	100.0	20	5	AAB13242	Human pep
100	22	100.0	20		AAB13235	Human lin
101	22	100.0	20	7	ADD93639	Streptoco
102	22	100.0	20	7	ADD93661	Streptoco
103	22	100.0	21	3	AAW53348	Nephila c
104	22	100.0	21	4	AAY59072	N. clavip
105	22	100.0	21		AAB69494	Synthetic
106	22	100.0	21	6	AAB47107	Human PrP
107	22	100.0	21	6	AAO16083	Mouse neu
108	22	100.0	21	6	AAO16080	Human neu
109	22	100.0	21	6	ABB82634	Human pri
110	22	100.0	21	6	ABU79034	Prion pro
111	22	100.0	21	7	ADC59529	Prion pep
112	22	100.0	21	7	ADC52086	Mouse pri
113	22	100.0	21	7	ABW00168	Prion (Pr
114	22	100.0	21	7	ADJ88131	Human PrP
115	22	100.0	21	8	ADJ88135	Mouse PrP
116	22	100.0	21	8	ADN00696	Human Pri
117	22	100.0	21	8	ADP44315	Chaperone
118	22	100.0	21	8	ADP44324	Chaperone
119	22	100.0	21	8	ADP44325	Chaperone
120	22	100.0	21	8	ADP44320	Chaperone
121	22	100.0	21	8	ADP44314	Chaperone
122	22	100.0	23	2	AAW76544	HIV-1 TAT
123	22	100.0	23	2	AAW76550	HIV-1 TAT
124	22	100.0	23	2	AAW76558	HIV-1 TAT
125	22	100.0	23	2	AAW76552	HIV-1 TAT
126	22	100.0	23	2	AAW76559	HIV-1 TAT
127	22	100.0	23	3	AAB14995	Amino aci
128	22	100.0	23	4	AAM21563	Peptide #
129	22	100.0	23	4	ABB43915	Peptide #
130	22	100.0	23	4	AAM37837	Peptide #
131	22	100.0	23	4	ABB26833	Protein #
132	22	100.0	23	4	AAM77641	Human bon
133	22	100.0	23	4	AAE12273	Mycobacte
134	22	100.0	23	4	AAM64905	Human bra
135	22	100.0	23	4	AAB82099	Hamster P
136	22	100.0	23	5	ABG59290	Human liv
137	22	100.0	23	5	ABG46673	Human pep
138	22	100.0	25	2	AAE15590	Hamster P
139	22	100.0	25	2	AAY59101	N. clavip
140	22	100.0	26	2	AAW76547	HIV-1 TAT
141	22	100.0	26	2	AAW76561	HIV-1 TAT
142	22	100.0	26	2	AAW76545	HIV-1 TAT
143	22	100.0	27	3	AAW76562	HIV-1 TAT
144	22	100.0	27	3	AAY59110	N. clavip
145	22	100.0	27	3	AAY59118	N. clavip
146	22	100.0	27	3	AAY59122	N. clavip
147	22	100.0	27	3	AAY59114	N. clavip
148	22	100.0	27	3	AAY51199	Human SCA
149	22	100.0	27	4	AAB15000	Amino aci
150	22	100.0	27	4	AAB82102	Hamster P
151	22	100.0	27	4	AAE15593	Hamster P
152	22	100.0	27	3	ADO08765	Novel sur
153	22	100.0	28	3	AAR64328	HSV L/ST
154	22	100.0	28	3	AAY59113	N. clavip
155	22	100.0	28	3	AAY59106	N. clavip
156	22	100.0	28	3	AAY59103	N. clavip
157	22	100.0	28	3	ABB04559	Hepatitis
158	22	100.0	29	2	AAR36788	Prion pro
159	22	100.0	29	2	AAY53550	Lipopepti
160	22	100.0	29	3	AAB10403	Pseudoman
161	22	100.0	29	3	AAB10837	Multivale
162	22	100.0	29	4	AAB14997	Amino aci
163	22	100.0	29	4	ABB41171	Peptide #
164	22	100.0	29	4	AAM34950	Peptide #
165	22	100.0	29	4	AAM74833	Human bon
166	22	100.0	29	4	AAM62031	Human bra
167	22	100.0	29	4	AAB82101	Hamster P
168	22	100.0	29	4	ABG56614	Human liv
169	22	100.0	29	4	ABG02689	Novel hum
170	22	100.0	29	5	AAE15592	Hamster P
171	22	100.0	30	3	AAY59111	N. clavip
172	22	100.0	30	3	AAY59116	N. clavip
173	22	100.0	30	3	AAY59121	N. clavip
174	22	100.0	30	3	AAY59124	N. clavip
175	22	100.0	30	3	AAY59104	N. clavip
176	22	100.0	30	3	AAY59123	N. clavip
177	22	100.0	30	5	ABB79705	Extracell
178	22	100.0	31	3	AAY59109	N. clavip
179	22	100.0	31	3	AAG55811	Arabidops
180	22	100.0	31	4	ABB38864	Peptide #
181	22	100.0	31	4	AAM32339	Peptide #
182	22	100.0	31	4	ABB23868	Protein #
183	22	100.0	31	4	AAM72075	Human bon
184	22	100.0	31	4	AAM59511	Human bra
185	22	100.0	31	4	ABG53761	Human liv
186	22	100.0	31	5	ABG41891	Human pep
187	22	100.0	31	7	ADD24215	Human pri
188	22	100.0	32	3	AAY59107	N. clavip
189	22	100.0	32	4	AAB91009	Somatosta
190	22	100.0	33	3	AAR12613	HIV-1 p17
191	22	100.0	33	2	AAR12623	HIV-1 p17
192	22	100.0	33	2	AAR36789	Prion pro
193	22	100.0	33	2	AAR36787	Prion pro
194	22	100.0	33	2	AAW17683	Prion pro
195	22	100.0	33	2	AAW53350	Nephila c
196	22	100.0	33	2	AAW53349	Nephila c
197	22	100.0	33	2	AAW70279	Generic p
198	22	100.0	33	3	AAY59073	N. clavip
199	22	100.0	33	3	AAY59074	N. clavip
200	22	100.0	33	3	AAB14996	Amino aci

ALIGNMENTS

RESULT 1
AAY42597
ID   AAY42597 standard; peptide; 6 AA.
XX
AC   AAY42597;
XX
DT   10-JAN-2000 (first entry)
XX
DE   Human IgE variant fragment.
XX
KW   Immunoglobulin E; IgE; antagonist; FcepsilonRI receptor; human; bds;
KW   receptor-binding; binding determinant sequence; anti-IgE antibody;
KW   allergic disease.
XX
OS   Homo sapiens.
XX
PN   US5965709-A.
XX
PD   12-OCT-1999.
XX
PF   21-APR-1994;   94US-00232539.
XX
PR   14-AUG-1991;   91US-00744768.
PR   07-JAN-1994;   94US-00178583.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Jardieu PM, Presta LG;
XX
DR   WPI; 1999-579941/49.
XX
PT   Immunoglobulin E variants as peptide antagonists useful for raising and
PT   screening anti-immunoglobulin E (IgE) antibodies, in the isolation and
PT   purification of FcepsilonRI receptor and in the treatment of allergic
PT   diseases.
XX
PS   Example 1; Col 35-36; 37pp; English.
XX
CC   The invention provides immunoglobulin E (IgE) antagonists comprising one

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 29, 2004, 07:44:37 ; Search time 37 Seconds
                                      (without alignments)
                                      8.962 Million cell updates/sec

Title: HOLLY-9
Perfect score: 22
Sequence: 1 aaaag 5

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database : Issued Patents AA:*
   1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
   2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
   3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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   5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
   6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	100.0	6	2	US-08-232-539D-31	Sequence 31, Appl
2	22	100.0	6	3	US-08-466-151-36	Sequence 36, Appl
3	22	100.0	6	3	US-09-128-450-3	Sequence 3, Appl
4	22	100.0	6	3	US-08-466-163B-36	Sequence 36, Appl
5	22	100.0	6	3	US-09-823-494-3	Sequence 3, Appli
6	22	100.0	6	4	US-09-802-096-36	Sequence 36, Appl
7	22	100.0	7	2	US-09-802-077-36	Sequence 36, Appl
8	22	100.0	7	2	US-08-442-461D-33	Sequence 33, Appl
9	22	100.0	8	2	US-08-612-785B-17	Sequence 17, Appl
10	22	100.0	8	3	US-09-128-450-1	Sequence 1, Appli
11	22	100.0	8	3	US-08-617-267C-17	Sequence 17, Appl
12	22	100.0	8	4	US-09-823-494-1	Sequence 1, Appli
13	22	100.0	8	4	US-09-367-572-4	Sequence 4, Appli
14	22	100.0	10	1	US-08-463-862-9	Sequence 9, Appli
15	22	100.0	10	1	US-08-458-887-9	Sequence 9, Appli
16	22	100.0	11	6	5178861-16	Patent No. 5178861
17	22	100.0	12	2	US-08-630-645-23	Sequence 23, Appl
18	22	100.0	12	2	US-09-149-934-5	Sequence 5, Appli
19	22	100.0	12	4	US-08-766-596A-23	Sequence 23, Appl
20	22	100.0	12	5	PCT-US96-10220-23	Sequence 23, Appl
21	22	100.0	14	1	US-08-556-823-3	Sequence 3, Appli
22	22	100.0	14	1	US-08-556-823-4	Sequence 4, Appli
23	22	100.0	14	4	US-08-766-596A-34	Sequence 34, Appl
24	22	100.0	14	4	US-09-073-009-101	Sequence 101, Appl
25	22	100.0	14	4	US-09-073-010-101	Sequence 101, App
26	22	100.0	16	2	US-08-308-494A-2	Sequence 2, Appli
27	22	100.0	18	1	US-08-240-712-33	Sequence 33, Appl
28	22	100.0	18	1	US-08-443-890-33	Sequence 33, Appl
29	22	100.0	18	3	US-09-053-617A-1	Sequence 1, Appli
30	22	100.0	18	3	US-09-628-588-1	Sequence 1, Appli
31	22	100.0	19	1	US-08-556-823-5	Sequence 5, Appli
32	22	100.0	19	1	US-08-244-701B-3	Sequence 3, Appli
33	22	100.0	19	3	US-08-244-701B-5	Sequence 5, Appli
34	22	100.0	19	3	US-09-076-721-3	Sequence 3, Appli
35	22	100.0	19	3	US-09-076-721-5	Sequence 5, Appli
36	22	100.0	21	2	US-08-425-069-5	Sequence 5, Appli
37	22	100.0	21	2	US-08-317-844B-5	Sequence 5, Appli
38	22	100.0	21	4	US-08-556-978B-43	Sequence 43, Appl
39	22	100.0	22	1	US-08-766-596A-35	Sequence 35, Appl
40	22	100.0	23	1	US-08-847-176-5	Sequence 5, Appli
41	22	100.0	23	2	US-08-847-176-12	Sequence 12, Appl
42	22	100.0	23	2	US-08-847-176-17	Sequence 17, Appl
43	22	100.0	23	3	US-08-847-176-18	Sequence 18, Appl
44	22	100.0	23	3	US-09-128-450-7	Sequence 7, Appli
45	22	100.0	23	3	US-08-556-978B-49	Sequence 49, Appl
46	22	100.0	23	3	US-09-823-494-7	Sequence 7, Appli
47	22	100.0	24	3	US-08-556-978B-55	Sequence 55, Appl
48	22	100.0	25	2	US-08-425-069-38	Sequence 38, Appl
49	22	100.0	25	2	US-08-317-844B-38	Sequence 38, Appl
50	22	100.0	26	2	US-08-847-176-6	Sequence 6, Appli
51	22	100.0	26	2	US-08-847-176-8	Sequence 8, Appli
52	22	100.0	26	2	US-08-847-176-20	Sequence 20, Appl
53	22	100.0	26	2	US-08-847-176-21	Sequence 21, Appl
54	22	100.0	26	2	US-08-847-176-22	Sequence 22, Appl
55	22	100.0	27	1	US-08-425-069-47	Sequence 47, Appl
56	22	100.0	27	1	US-08-425-069-51	Sequence 51, Appl
57	22	100.0	27	1	US-08-425-069-55	Sequence 55, Appl
58	22	100.0	27	2	US-08-425-069-59	Sequence 59, Appl
59	22	100.0	27	2	US-08-317-844B-47	Sequence 47, Appl
60	22	100.0	27	2	US-08-317-844B-51	Sequence 51, Appl
61	22	100.0	27	2	US-08-317-844B-55	Sequence 55, Appl
62	22	100.0	27	3	US-08-317-844B-59	Sequence 59, Appl
63	22	100.0	27	3	US-08-128-450-10	Sequence 10, Appl
64	22	100.0	27	1	US-08-556-978B-29	Sequence 29, Appl
65	22	100.0	27	3	US-08-556-978B-92	Sequence 92, Appl
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67	22	100.0	27	3	US-09-823-494-10	Sequence 10, Appl
68	22	100.0	27	4	US-09-684-843A-11	Sequence 11, Appl
69	22	100.0	28	1	US-08-425-069-40	Sequence 40, Appl
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71	22	100.0	28	2	US-08-425-069-50	Sequence 50, Appl
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77	22	100.0	29	2	US-08-244-701B-51	Sequence 51, Appl
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82	22	100.0	29	3	US-09-076-721-51	Sequence 51, Appl
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116	22	100.0	33	US-09-823-494-8	3	Sequence 8, Appl
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119	22	100.0	33	US-09-823-494-29	3	Sequence 29, Appl
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121	22	100.0	33	US-09-076-721-2	3	Sequence 2, Appl
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164	22	100.0	50	US-09-126-121-18	3	Sequence 18, Appl
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166	22	100.0	52	US-09-474-507-3	4	Sequence 3, Appli
167	22	100.0	55	US-08-209-747-10	1	Sequence 10, Appl
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175	22	100.0	58	US-09-270-767-42949	4	Sequence 42949, A
176	22	100.0	60	US-09-248-796A-27598	4	Sequence 27598, A
177	22	100.0	61	US-09-270-767-59888	4	Sequence 59888, A
178	22	100.0	64	US-09-248-335-8	3	Sequence 8, Appli
179	22	100.0	73	US-09-621-976-6591	4	Sequence 6591, Ap
180	22	100.0	74	US-09-621-976-4915	4	Sequence 4915, Ap
181	22	100.0	76	US-09-428-082B-374	4	Sequence 374, App
182	22	100.0	79	US-09-187-999-25	4	Sequence 25, Appl
183	22	100.0	80	US-08-209-747-12	1	Sequence 12, Appl
184	22	100.0	80	US-08-458-298-12	1	Sequence 12, Appl
185	22	100.0	83	US-09-513-999C-7280	4	Sequence 7280, Ap
186	22	100.0	84	US-09-489-039A-12508	4	Sequence 12508, A
187	22	100.0	87	US-09-450-072-74	3	Sequence 74, Appl
188	22	100.0	87	US-09-351-348-74	4	Sequence 74, Appl
189	22	100.0	87	US-09-621-976-7020	4	Sequence 7020, Ap
190	22	100.0	88	US-09-270-767-37480	4	Sequence 37480, A
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192	22	100.0	93	US-09-621-976-4468	4	Sequence 4468, Ap
193	22	100.0	93	US-09-270-767-56856	4	Sequence 56856, A
194	22	100.0	95	US-09-621-976-4670	4	Sequence 4670, Ap
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199	22	100.0	99	US-09-073-009-32	4	Sequence 32, Appl
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ALIGNMENTS

RESULT 1
US-08-232-539D-31
; Sequence 31, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: IgE Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/232,539D
;   FILING DATE: 21-Apr-1994
;   CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/178583
;   FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/744768
;   FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
;   NAME: Svoboda, Craig G.
;   REGISTRATION NUMBER: 39,044
;   REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-1489
;   TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 6 amino acids

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OM protein - protein search, using sw model

            Copyright   GenCore version 5.1.6
                        (c) 1993 - 2004 Compugen Ltd.

Run on:     November 29, 2004, 07:44:37 ; Search time 188 Seconds
                                           (without alignments)
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Title:          HOLLY-9
Perfect score:  22
Sequence:       1 aaaag 5
Scoring table:  BLOSUM62
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Searched:       1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters:   1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 200 summaries

Database :        UniProt_02:*
                  1: uniprot_sprot:*
                  2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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3	22	100.0	26	2	Q9UPD8	Q9upd8 homo sapien
4	22	100.0	30	2	Q9QV43	Q9qv43 rattus sp.
5	22	100.0	33	2	Q6JUZ3	Q6juz3 ovis aries
6	22	100.0	33	2	Q6JUZ6	Q6juz6 ovis aries
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8	22	100.0	33	2	AAQ81747	Aaq81747 ovis arie
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79	22	100.0	71	2	AAS53397	Aas53397 ashbya go
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124	100.0	22	Q7XIW3	Q7xiw3	oryza sativ
125	100.0	22	Q84XF0	Q84xf0	oryza sativ
126	100.0	22	Q8L4P7	Q8l4p7	oryza sativ
127	100.0	22	Q8S0E6	Q8s0e6	oryza sativ
128	100.0	22	BAD07961	Bad07961	oryza sat
129	100.0	22	AAS98441	Aas98441	oryza sat
130	100.0	22	Q8LRA5	Q8lra5	oryza sativ
131	100.0	22	Q9XIX4	Q9xix4	oryza sativ
132	100.0	22	Q7TVE8	Q7tve8	mycobacteri
133	100.0	22	Q7D4N3	Q7d4n3	mycobacteri
134	100.0	22	Q9WSA4	Q9wsa4	human immun
135	100.0	22	CAE55650	Cae55650	mycobacte
136	100.0	22	PUR9_CHRVI	Q46480	c bifunctio
137	100.0	22	Q6BU54	Q6bus4	debaryomyce
138	100.0	22	Q8LNB9	Q8lnb9	oryza sativ
139	100.0	22	Q8N160	Q8n160	homo sapien
140	100.0	22	Q6L5I8	Q6l5i8	oryza sativ
141	100.0	22	Q9WW18	Q9ww18	pseudomonas
142	100.0	22	Q98NI1	Q98ni1	rhizobium l
143	100.0	22	AAT39211	Aat39211	oryza sat
144	100.0	22	Q6IGY1	Q6igy1	drosophila
145	100.0	22	O96796	O96796	skeletonema
146	100.0	22	Q84SW6	Q84sw6	oryza sativ
147	100.0	22	Q9M4Y6	Q9m4y6	oryza sativ
148	100.0	22	Q9WSA1	Q9wsa1	human immun
149	100.0	22	P93427	P93427	oryza sativ
150	100.0	22	Q6D780	Q6d780	erwinia car
151	100.0	22	Q6K4B4	Q6k4b4	oryza sativ
152	100.0	22	Q6Z606	Q6z606	oryza sativ
153	100.0	22	Q84PU8	Q84pu8	oryza sativ
154	100.0	22	Q6TV92	Q6tv92	bovine papu
155	100.0	22	BAC99677	Bac99677	oryza sat
156	100.0	22	AAR98453	Aar98453	bovine pa
157	100.0	22	BAD22255	Bad22255	oryza sat
158	100.0	22	Q9NTR9	Q9ntr9	homo sapien
159	100.0	22	Q7PNA9	Q7pna9	anopheles g
160	100.0	22	Q64827	Q64827	human adeno
161	100.0	22	Q8QS40	Q8qs40	chimpanzee
162	100.0	22	MRK0_RAT	P20468	rattus norv
163	100.0	22	Q6H724	Q6h724	oryza sativ
164	100.0	22	Q8XWU6	Q8xwu6	ralstonia s
165	100.0	22	YBIU_ECOLI	P41038	escherichia
166	100.0	22	Q7XVE5	Q7xve5	oryza sativ
167	100.0	22	Q6H751	Q6h751	oryza sativ
168	100.0	22	Q9FTX8	Q9ftx8	oryza sativ
169	100.0	22	Q6EN67	Q6en67	oryza sativ
170	100.0	22	Q7AGC3	Q7agc3	escherichia
171	100.0	22	Q8G2Q4	Q8g2q4	brucella su
172	100.0	22	Q8X7X2	Q8x7x2	escherichia
173	100.0	22	Q8XFN7	Q8xfn7	salmonella
174	100.0	22	Q8YF68	Q8yf68	brucella me
175	100.0	22	Q7CQW3	Q7cqw3	salmonella
176	100.0	22	Q6YX56	Q6yx56	oryza sativ
177	100.0	22	Q6Z3Q2	Q6z3q2	oryza sativ

#	Len	%	Score	DB	AC	ID	Organism
178	22	100.0	87	2	Q6ZJQ5	Q6zjq5	oryza sativ
179	22	100.0	87	2	Q93VJ3	Q93vj3	oryza sativ
180	22	100.0	87	2	BAC84116	Bac84116	oryza sat
181	22	100.0	87	2	BAD03847	Bad03847	oryza sat
182	22	100.0	87	2	BAD05241	Bad05241	oryza sat
183	22	100.0	88	1	RS20_STRCO	Q9rdm3	streptomyce
184	22	100.0	88	2	P91335	P91335	caenorhabdi
185	22	100.0	88	2	Q7XVI7	Q7xvi7	oryza sativ
186	22	100.0	88	2	Q7Y1S2	Q7y1s2	zea mays (m
187	22	100.0	88	2	Q7Y1S4	Q7y1s4	zea mays (m
188	22	100.0	88	2	Q6H4D7	Q6h4d7	oryza sativ
189	22	100.0	88	2	Q9LIX6	Q9lix6	oryza sativ
190	22	100.0	88	2	Q82BZ4	Q82bz4	streptomyce
191	22	100.0	88	2	Q92RU0	Q92ru0	rhizobium m
192	22	100.0	89	2	Q9N9Q1	Q9n9q1	leishmania
193	22	100.0	89	2	Q84Z20	Q84z20	oryza sativ
194	22	100.0	89	2	Q73SS2	Q73ss2	mycobacteri
195	22	100.0	89	2	Q6FB75	Q6fb75	acinetobact
196	22	100.0	89	2	Q709T8	Q709t8	human immun
197	22	100.0	89	2	AAS06551	Aas06551	mycobacte
198	22	100.0	89	2	CAE54783	Cae54783	human imm
199	22	100.0	90	2	Q7S7Q0	Q7s7q0	neurospora
200	22	100.0	90	2	Q8H4N9	Q8h4n9	oryza sativ

ALIGNMENTS

RESULT 1
UN04_PINPS
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ID   UN04_PINPS     STANDARD;      PRT;    15 AA.
AC   P81673;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Unknown protein from 2D-PAGE of needles (N143) (Fragment).
OS   Pinus pinaster (Maritime pine).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Coniferophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX   NCBI_TaxID=71647;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Needle;
RX   MEDLINE=99274088; PubMed=10344291;
RA   Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA   Frigerio J.-M., Plomion C.;
RT   "Separation and characterization of needle and xylem maritime pine
RT   proteins.";
RL   Electrophoresis 20:1098-1108(1999).
CC   -!- INDUCTION: By water stress.
CC   -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC       protein is: 6.2, its MW is: 21 kDa.
KW   Direct protein sequencing.
FT   NON_TER       1      1
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;   1489 MW;   CE4DB5E99308227A CRC64;

Query Match             100.0%;   Score 22;   DB 1;   Length 15;
Best Local Similarity   100.0%;   Pred. No. 7.6e+02;
Matches    5;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy        1 AAAAG 5
            |||||
Db        7 AAAAG 11
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RESULT 2
Q9ZOJ2
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ID   Q9ZOJ2;                       PRELIMINARY;      PRT;    16 AA.
AC   Q9ZOJ2;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
```

```
                GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:   November 29, 2004, 07:44:37 ; Search time 39 Seconds
                                         (without alignments)
                                         12.335 Million cell updates/sec

Title:           HOLLY-9
Perfect score:   22
Sequence:        1 aaaag 5

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters:    283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   PIR.79:*
        1: pir1:*
        2: pir2:*
        3:· pir3:*
        4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Match	Query	Length	DB	ID	Description
1	22	100.0	22	19	2	B43978	urotensin I precur
2	22	100.0	22	35	2	A61375	basic fibroblast g
3	22	100.0	22	54	2	E70787	hypothetical glyci
4	22	100.0	22	54	2	C71570	hypothetical prote
5	22	100.0	22	54	2	T29665	hypothetical prote
6	22	100.0	22	57	2	T03654	glyceraldehyde-3-p
7	22	100.0	22	57	2	AG3105	conserved hypothet
8	22	100.0	22	66	2	AB3503	LSU ribosomal prot
9	22	100.0	22	66	2	S22529	cold-regulated pro
10	22	100.0	22	67	2	F97389	50S ribosomal prot
11	22	100.0	22	67	2	AG2607	50S ribosomal prot
12	22	100.0	22	70	2	S58932	DNA-directed RNA p
13	22	100.0	22	74	2	T47211	ccg-6 protein [imp
14	22	100.0	22	76	2	A69033	hypothetical prote
15	22	100.0	22	77	2	F70598	probable PE protei
16	22	100.0	22	86	2	AD0600	probable exported
17	22	100.0	22	86	2	B64817	ybiJ protein precu
18	22	100.0	22	86	2	B85589	hypothetical prote
19	22	100.0	22	86	2	H90738	hypothetical prote
20	22	100.0	22	86	2	AC3459	hypothetical prote
21	22	100.0	22	88	2	T34429	hypothetical prote
22	22	100.0	22	90	2	JN0492	hypothetical 9.7K
23	22	100.0	22	92	2	RIPGS	somatostatin I pre
24	22	100.0	22	92	2	B87456	ribosomal protein
25	22	100.0	22	93	2	C82650	hypothetical prote
26	22	100.0	22	97	2	T30458	hypothetical prote
27	22	100.0	22	98	2	B70568	probable PE protei
28	22	100.0	22	98	2	D75519	hypothetical prote
29	22	100.0	22	99	1	R6MXL2	ribosomal protein
30	22	100.0	22	99	2	A70930	probable PE protei
31	22	100.0	22	99	2	F70929	probable PE protei
32	22	100.0	22	100	2	S20482	hypothetical prote
33	22	100.0	22	101	2	A33351	H+-transporting tw
34	22	100.0	22	102	2	D90203	ATP synthase subun
35	22	100.0	22	104	2	S45400	probable membrane
36	22	100.0	22	104	2	F83370	hydrogen cyanide s
37	22	100.0	22	106	1	R8BY2B	acidic ribosomal p
38	22	100.0	22	106	2	T52147	ribosomal protein
39	22	100.0	22	109	2	T04144	DNA binding protei
40	22	100.0	22	110	1	R6BY22	60s acidic ribosom
41	22	100.0	22	110	1	R6BYP3	60s acidic ribosom
42	22	100.0	22	110	2	JC2260	Streptoverticilliu
43	22	100.0	22	111	1	R8SS12	ribosomal protein
44	22	100.0	22	111	1	S43115	acidic ribosomal p
45	22	100.0	22	111	2	S41866	acidic ribosomal p
46	22	100.0	22	111	2	D75566	conserved hypothet
47	22	100.0	22	111	2	E98181	hypothetical prote
48	22	100.0	22	112	1	R6UT2B	acidic ribosomal p
49	22	100.0	22	112	2	S35440	acidic ribosomal p
50	22	100.0	22	112	2	T36440	hypothetical prote
51	22	100.0	22	113	1	R6FFP2	acidic ribosomal p
52	22	100.0	22	113	2	S43109	acidic ribosomal p
53	22	100.0	22	113	2	T30041	hypothetical prote
54	22	100.0	22	113	2	T22851	hypothetical prote
55	22	100.0	22	115	2	G87300	dihydroneopterin a
56	22	100.0	22	116	1	A28968	somatostatin I pre
57	22	100.0	22	116	1	RIBOS1	somatostatin precu
58	22	100.0	22	116	1	RIHUS1	somatostatin I pre
59	22	100.0	22	116	2	S20630	somatostatin precu
60	22	100.0	22	116	1	IPAF	insulin precursor
61	22	100.0	22	117	2	H84651	hypothetical prote
62	22	100.0	22	119	2	T36513	hypothetical prote
63	22	100.0	22	120	2	PH0083	neuroglian, long c
64	22	100.0	22	121	2	D86783	50S ribosomal prot
65	22	100.0	22	123	2	A34172	traJ protein - Esc
66	22	100.0	22	124	2	H81005	adhesin complex pr
67	22	100.0	22	126	1	T16727	hypothetical prote
68	22	100.0	22	129	2	T31200	hypothetical prote
69	22	100.0	22	129	2	T00003	pepH protein - Aci
70	22	100.0	22	130	2	S41571	blasticidin-S deam
71	22	100.0	22	130	2	H81684	ribosomal protein
72	22	100.0	22	130	2	A71530	ribosomal protein
73	22	100.0	22	132	1	MTON1K	melanin-concentrat
74	22	100.0	22	132	1	MTON2K	melanin-concentrat
75	22	100.0	22	132	2	S34654	melanin-concentrat
76	22	100.0	22	132	2	S34653	melanin-concentrat
77	22	100.0	22	132	2	A32910	melanin-concentrat
78	22	100.0	22	132	2	B32910	hypothetical prote
79	22	100.0	22	132	2	B85092	homeotic protein L
80	22	100.0	22	132	2	S43488	hypothetical prote
81	22	100.0	22	134	2	A26986	probable cytochrom
82	22	100.0	22	134	2	C82030	MAPEG family prote
83	22	100.0	22	135	2	F87264	hypothetical prote
84	22	100.0	22	135	2	G72601	hypothetical prote
85	22	100.0	22	136	2	AB2388	cytochrome c5 PA53
86	22	100.0	22	136	2	D82982	hypothetical prote
87	22	100.0	22	137	2	H84218	hypothetical prote
88	22	100.0	22	138	2	S13332	probable membrane
89	22	100.0	22	138	2	C87389	probable V-type AT
90	22	100.0	22	139	2	A81938	probable transcrip
91	22	100.0	22	140	2	C71326	hypothetical prote
92	22	100.0	22	141	2	C83007	dehydrin 9 - barle
93	22	100.0	22	142	2	E95263	hypothetical prote
94	22	100.0	22	143	1	S05543	hypothetical prote
95	22	100.0	22	144	2	D72517	somatostatin I pre
96	22	100.0	22	145	2	H87436	ribosomal protein
97	22	100.0	22	146	2	T10511	hypothetical prote
98	22	100.0	22	147	2	H72548	hypothetical prote
99	22	100.0	22	150	2	S69530	probable PE protei
100	22	100.0	22	151	1	S70787	curlin nucleator p
101	22	100.0	22	151	2	C90806	minor curlin subun
102	22	100.0	22	151	2	G85665	curlin minor chain

103	22	100.0	H87407	2	conserved hypothet
104	22	100.0	E70615	2	hypothetical prote
105	22	100.0	T49895	2	oleosin-like prote
106	22	100.0	T03463	2	hypothetical prote
107	22	100.0	T21364	2	hypothetical prote
108	22	100.0	T02034	2	early light-induce
109	22	100.0	T33892	2	hypothetical prote
110	22	100.0	C70882	2	hypothetical prote
111	22	100.0	T35329	2	probable DNA-bindi
112	22	100.0	H75028	2	probable H+-transp
113	22	100.0	S35787	2	US9 protein - bovi
114	22	100.0	PN0614	2	superoxide dismuta
115	22	100.0	T45343	2	hypothetical prote
116	22	100.0	D71214	2	hypothetical prote
117	22	100.0	H75471	2	hypothetical prote
118	22	100.0	T17031	2	fimbriata-associat
119	22	100.0	C70746	2	hypothetical prote
120	22	100.0	AD3624	2	hypothetical prote
121	22	100.0	A45119	2	basic helix-loop-h
122	22	100.0	T04903	2	iron-sulfur cofact
123	22	100.0	A55438	2	transcription fact
124	22	100.0	T02036	2	early light-induce
125	22	100.0	S72171	2	helix-loop-helix p
126	22	100.0	G70587	2	hypothetical prote
127	22	100.0	H84191	2	hypothetical prote
128	22	100.0	F81038	2	probable shikimate
129	22	100.0	T51122	2	crtK protein (impo
130	22	100.0	T51469	2	glycine/proline-ri
131	22	100.0	T02869	2	globulin 1 precurs
132	22	100.0	F84338	2	hypothetical prote
133	22	100.0	S72704	2	Lepb1170_C2_203 pr
134	22	100.0	I48752	2	gene RXRbeta1 prot
135	22	100.0	A34690	2	DNA-binding protei
136	22	100.0	AF0460	2	probable membrane
137	22	100.0	I49069	2	A+U-rich RNA-bindi
138	22	100.0	G87307	2	hypothetical prote
139	22	100.0	E70069	2	hypothetical prote
140	22	100.0	T06094	2	hypothetical prote
141	22	100.0	E75340	2	conserved hypothet
142	22	100.0	B88637	2	protein W09G12.6 [
143	22	100.0	G75594	2	cobinamide kinase/
144	22	100.0	T35750	2	hypothetical prote
145	22	100.0	C61600	2	segmentation prote
146	22	100.0	T25598	2	hypothetical prote
147	22	100.0	S06616	2	chorion protein s1
148	22	100.0	JC7876	2	prion protein homo
149	22	100.0	F70586	2	hypothetical prote
150	22	100.0	T02974	2	probable DNA bindi
151	22	100.0	S57778	2	oleosin 1 - barley
152	22	100.0	D87605	2	transcription regu
153	22	100.0	G72783	2	hypothetical prote
154	22	100.0	D83344	2	hypothetical prote
155	22	100.0	C82029	2	probable adhesin c
156	22	100.0	T35736	2	hypothetical prote
157	22	100.0	S49755	2	adenine phosphorib
158	22	100.0	A34014	2	integrin alpha-3 c
159	22	100.0	A48834	2	basic fibroblast g
160	22	100.0	G69932	2	hypothetical prote
161	22	100.0	E70840	2	probable dehydrata
162	22	100.0	H83151	2	hypothetical prote
163	22	100.0	B87460	2	phosphoribosylglyc
164	22	100.0	T36959	2	hypothetical prote
165	22	100.0	A70583	2	probable resolvase
166	22	100.0	H70672	2	probable resolvase
167	22	100.0	T28653	2	resolvase - Pseudo
168	22	100.0	S24228	2	BHV-1 protein homo
169	22	100.0	A28201	2	cytochrome b-245 a
170	22	100.0	H95297	2	probable allantoin
171	22	100.0	E83895	2	transcription regu
172	22	100.0	S26493	2	translation initia
173	22	100.0	F84264	2	sulfite oxidase ho
174	22	100.0	C32998	2	chorion protein S1
175	22	100.0	T49450	2	hypothetical prote

176	22	100.0	B71295	2	probable cell divi
177	22	100.0	E84189	2	hypothetical prote
178	22	100.0	B87340	2	transcription regu
179	22	100.0	TVHUC2	1	GTP-binding protei
180	22	100.0	D81116	2	RNA methyltransfer
181	22	100.0	T35012	2	probable transcrip
182	22	100.0	H70648	2	probable regulator
183	22	100.0	G84530	2	probable RING-H2 z
184	22	100.0	B87609	2	hypothetical prote
185	22	100.0	F84274	2	halocyanin precurs
186	22	100.0	G83854	2	hypothetical prote
187	22	100.0	S76279	2	hypothetical prote
188	22	100.0	AC2950	2	transcription regu
189	22	100.0	G87507	2	glutathione S-tran
190	22	100.0	D75556	2	phosphoribosylanth
191	22	100.0	G81169	2	N-(5'-phosphoribos
192	22	100.0	T30625	2	hypothetical prote
193	22	100.0	E86221	2	hypothetical prote
194	22	100.0	H75626	2	DNA-binding respon
195	22	100.0	G69321	2	conserved hypothet
196	22	100.0	E86976	2	probable guanylate
197	22	100.0	F70546	2	hypothetical prote
198	22	100.0	D97502	2	hypothetical prote
199	22	100.0	AH2720	2	RhtB family transp
200	22	100.0	H70687	2	hypothetical prote

ALIGNMENTS

RESULT 1
B43978
urotensin I precursor - European flounder (fragment)
C;Species: Platichthys flesus (European flounder)
C;Date: 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change 18-Jun-1993
C;Accession: B43978
R;Conlon, J.M.; Arnold-Reed, D.E.; Balment, R.J.
Peptides 11, 891-895, 1990
A;Title: Urotensin I and its N-terminal flanking peptide from the flounder, Platichthys
A;Reference number: A43978
A;Accession: B43978
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <CON>

Query Match   100.0%;   Score 22;   DB 2;   Length 19;
Best Local Similarity   100.0%;   Pred. No. 97;
Matches   5;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy    1 AAAAG 5
          |||||
Db    1 AAAAG 5
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RESULT 2
A61375
basic fibroblast growth factor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Sep-1994
C;Accession: A61375
R;Powell, P.P.; Klagsbrun, M.
J. Cell. Physiol. 148, 202-210, 1991
A;Title: Three forms of rat basic fibroblast growth factor are made from a single mRNA
A;Reference number: A61375; MUID:91349212; PMID:1880150
A;Accession: A61375
A;Molecule type: mRNA
A;Residues: 1-35 <POW>
C;Genetics:
A;Start codon: AGG
C;Keywords: alternative initiators

Query Match   100.0%;   Score 22;   DB 2;   Length 35;

OM protein - protein search, using sw model

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Run on: November 29, 2004, 07:44:37 ; Search time 777 Seconds
                                         (without alignments)
                                         2.282 Million cell updates/sec

Title: HOLLY-9
Perfect score: 22
Sequence: 1 aaaag 5

Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 1575965

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                          SUMMARIES

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ALIGNMENTS

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;	APPLICANT: Presta, Leonard G.
;	TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
;	FILE REFERENCE: P0718P2C2US
;	CURRENT APPLICATION NUMBER: US/09/802,077
;	CURRENT FILING DATE: 2001-03-08
;	PRIOR APPLICATION NUMBER: US 08/405,617
;	PRIOR FILING DATE: 1995-03-15
;	PRIOR APPLICATION NUMBER: US 08/185,899
;	PRIOR FILING DATE: 1994-01-26
;	PRIOR APPLICATION NUMBER: PCT/US92/06860
;	PRIOR FILING DATE: 1992-08-14
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;	PRIOR FILING DATE: 1992-05-07
;	PRIOR APPLICATION NUMBER: US 07/744,768
;	PRIOR FILING DATE: 1991-08-14
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;	ORGANISM: Artificial sequence
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OM protein - protein search, using sw model

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Perfect score: 17
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Total number of hits satisfying chosen parameters: 2002273

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Post-processing: Minimum Match 0%
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(handwritten annotations:) SEQ ID 13 1-5 — with NKA repeat — with X (any a.a.)

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and is derived by analysis of the total score distribution.

SUMMARIES

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18	17	100.0	17	8	3	AAY69113	Aay69113 Subsequen
19	17	100.0	17	8	3	AAY69114	Aay69114 Subsequen
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21	17	100.0	17	8	3	AAY69115	Aay69115 Subsequen
22	17	100.0	17	8	3	AAY69130	Aay69130 Subsequen
23	17	100.0	17	8	3	AAY69141	Aay69141 Peptidomi
24	17	100.0	17	8	3	AAY69932	Aay69932 Human cyc
25	17	100.0	17	9	2	AAR66567	Aar66567 Cyclic gu
26	17	100.0	17	9	2	AAW00691	Aaw00691 Positive
27	17	100.0	17	9	2	AAW04637	Aaw04637 Null pept
28	17	100.0	17	9	2	AAY46647	Aay46647 Immunogen
29	17	100.0	17	9	2	AAY14988	Aay14988 Bovine cG
30	17	100.0	17	9	5	ABB97067	Abb97067 Human tum
31	17	100.0	17	9	6	ABP58411	Abp58411 Null pept
32	17	100.0	17	9	6	ABR09615	Abr09615 Human can
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35	17	100.0	17	9	6	ABR09797	Abr09797 Human can
36	17	100.0	17	9	6	ABR09386	Abr09386 Human can
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72	17	100.0	17	9	7	ABU64355	Abu64355 Human AAC
73	17	100.0	17	9	7	ADI15709	Adi15709 HLA-A2 re
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75	17	100.0	17	9	7	ADK24375	Adk24375 Human 98P
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77	17	100.0	17	9	7	ADK24381	Adk24381 Human 98P
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80	17	100.0	17	10	2	AAR05973	Aar05973 Somatic i
81	17	100.0	17	10	2	AAW41760	Aaw41760 Colony st
82	17	100.0	17	10	4	AAG97092	Aag97092 Human com
83	17	100.0	17	10	4	AAG95318	Aag95318 Human com
84	17	100.0	17	10	4	AAG96449	Aag96449 Human com
85	17	100.0	17	10	4	AAG94410	Aag94410 Human com
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87	17	100.0	17	10	5	ABG32275	Abg32275 Lysozyme
88	17	100.0	17	10	6	ABR09083	Abr09083 Human can
89	17	100.0	17	10	6	ABR09911	Abr09911 Human can
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91	17	100.0	17	10	6	ABR09101	Abr09101 Human can
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94	17	100.0	17	10	6	ABR09270	Abr09270 Human can
95	17	100.0	17	10	6	ABR09914	Abr09914 Human can
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97	17	100.0	17	10	6	ABR09475	Abr09475 Human can
98	17	100.0	17	10	6	ABR09695	Abr09695 Human can

99	100.0	17	10	6	ABR10114	Human can
100	100.0	17	10	6	ABR09471	Human can
101	100.0	17	10	6	ABR09679	Human can
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103	100.0	17	10	6	ABR09479	Human can
104	100.0	17	10	6	ABR09509	Human can
105	100.0	17	10	6	ABR10312	Human can
106	100.0	17	10	6	ABR09104	Human can
107	100.0	17	10	6	ABR09119	Human can
108	100.0	17	10	6	ABR09874	Human can
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110	100.0	17	10	6	ABR09489	Human can
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129	100.0	17	10	6	ABR10317	Human can
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131	100.0	17	10	7	ADD23764	Breast ca
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138	100.0	17	10	2	AAR08092	Antifreez
139	100.0	17	11	5	AAY69933	Human cyc
140	100.0	17	11	5	ABG31566	Lysozyme
141	100.0	17	11	5	AAU82656	BP protei
142	100.0	17	11	5	AAU82657	BP protei
143	100.0	17	11	6	AAE31824	Androgen
144	100.0	17	11	7	ADD15091	Peptide s
145	100.0	17	11	7	ADD15103	Peptide s
146	100.0	17	11	7	ADD15020	Peptide s
147	100.0	17	11	7	ADD15035	Peptide s
148	100.0	17	11	7	ADD15109	Peptide s
149	100.0	17	11	7	ADM09044	Canine im
150	100.0	17	11	8	ADK15579	Membrane
151	100.0	17	11	8	ADK17319	Human OCT
152	100.0	17	12	2	AAR67199	Bovine gl
153	100.0	17	12	2	AAR86663	GGF II tr
154	100.0	17	12	3	AAB29166	Peptide #
155	100.0	17	12	3	AAB29165	Peptide #
156	100.0	17	13	2	AAR81974	ORF encod
157	100.0	17	13	2	AAR97161	Conantoki
158	100.0	17	13	3	AAY05004	Tumour an
159	100.0	17	13	3	AAY99239	HLA class
160	100.0	17	13	6	AAE35589	Trojan an
161	100.0	17	13	6	ABU09119	Human Mad
162	100.0	17	13	6	ABU09121	Human Mad
163	100.0	17	13	7	ADC82726	CDR regio
164	100.0	17	13	7	ADF11998	Mycobacte
165	100.0	17	13	8	ADK65093	PPIc-inte
166	100.0	17	13	8	ADM31945	A-A' beta
167	100.0	17	13	8	ADN64954	HLA bindi
168	100.0	17	13	8	ADO24026	HBV epito
169	100.0	17	14	1	AAP83237	Epstein-B
170	100.0	17	14	2	AAR32947	Mastopara
171	100.0	17	14	2	AAR32963	Mastopara
172	100.0	17	14	3	AAY99243	HLA class
173	100.0	17	14	4	AAM98274	Human pep
174	100.0	17	14	4	AAM98023	Human pep
175	100.0	17	14	6	ABR82573	BID alpha
176	100.0	17	14	6	ABR82574	BID alpha
177	100.0	17	14	6	ABR82572	BID alpha
178	100.0	17	14	7	ABM74394	DNA clone
179	100.0	17	14	8	ADK01533	Hepatitis
180	100.0	17	15	2	AAR48075	C-termina
181	100.0	17	15	2	AAR56467	B. mori s
182	100.0	17	15	2	AAW32854	Mastopara
183	100.0	17	15	2	AAW73726	M. tuberc
184	100.0	17	15	2	AAW73727	M. tuberc
185	100.0	17	15	2	AAW87843	Human Bcl
186	100.0	17	15	2	AAW73837	M. tuberc
187	100.0	17	15	3	AAW73836	M. tuberc
188	100.0	17	15	3	AAY94596	Mycobacte
189	100.0	17	15	3	AAB29738	Phage dis
190	100.0	17	15	3	AAB10822	Expressio
191	100.0	17	15	3	AAB10823	Expressio
192	100.0	17	15	4	AAM98975	Vaccine r
193	100.0	17	15	4	AAU10758	LEPB pept
194	100.0	17	15	4	AAU08191	Mycobacte
195	100.0	17	15	4	AAU08192	Mycobacte
196	100.0	17	15	4	AAB74160	BCL2 BH1
197	100.0	17	15	5	ABG30957	Mycobacte
198	100.0	17	15	5	ABG30958	Mycobacte
199	100.0	17	15	6	ABR32580	Human can
200	100.0	17	15	6	ABR32684	Human can

ALIGNMENTS

RESULT 1
AAE20126
ID   AAE20126 standard; peptide; 6 AA.
XX
AC   AAE20126;
XX
DT   18-JUN-2002   (first entry)
XX
DE   Human TRIP leucine zipper peptide #1.
XX
KW   Human; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
KW   TRAF interacting protein; TRIP; cell activation; cell proliferation;
KW   cell death; therapy; cytostatic; leucine zipper.
XX
OS   Homo sapiens.
XX
PN   US6346605-B1.
XX
PD   12-FEB-2002.
XX
PF   31-MAR-1998;   98US-00052089.
XX
PR   01-APR-1997;   97US-0042293P.
PR   07-APR-1997;   97US-0042747P.
XX
PA   (UYRQ) UNIV ROCKEFELLER.
XX
PI   Lee SY, Choi Y;
XX
DR   WPI; 2002-225005/28.
XX
PT   New tumor necrosis factor receptor associated factor interacting protein,
PT   useful for inhibiting NF-kappa B activation, and for modulating signals
PT   responsible for cell activation, cell proliferation and cell death.
XX
PS   Example 2; Fig 2E; 37pp; English.
XX
CC   The present invention relates to a tumour necrosis factor (TNF) receptor
CC   associated factor (TRAF) interacting protein (TRIP), which is a regulator

OM protein - protein search, using sw model

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Run on: November 29, 2004, 08:02:06 ; Search time 21 Seconds
                                          (without alignments)
                                          15.790 Million cell updates/sec

Title: HOLLY-13
Perfect score: 17
Sequence: 1 xlaaa 5
Scoring table: BLOSUM62DX
                  Gapop 10.0 , Gapext 0.5
Searched: 478139 seqs, 6618000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 200 summaries

Database :   Issued_Patents_AA:*
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   6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	Pred.	DB	ID	Description
1	17	100.0	17	6	3	US-09-330-970-24	Sequence 24, Appl
2	17	100.0	17	6	3	US-09-330-970-38	Sequence 38, Appl
3	17	100.0	17	7	2	US-09-335-224B-14	Sequence 14, Appl
4	17	100.0	17	8	2	US-08-234-539D-43	Sequence 43, Appl
5	17	100.0	17	8	2	US-08-464-025A-17	Sequence 17, Appl
6	17	100.0	17	8	3	US-08-466-151-25	Sequence 25, Appl
7	17	100.0	17	8	3	US-08-466-151-58	Sequence 58, Appl
8	17	100.0	17	8	3	US-08-466-163B-25	Sequence 25, Appl
9	17	100.0	17	8	4	US-08-466-163B-58	Sequence 58, Appl
10	17	100.0	17	8	4	US-09-043-816E-15	Sequence 15, Appl
11	17	100.0	17	8	4	US-09-802-096-25	Sequence 25, Appl
12	17	100.0	17	8	4	US-09-802-096-58	Sequence 58, Appl
13	17	100.0	17	8	4	US-09-802-077-25	Sequence 25, Appl
14	17	100.0	17	8	4	US-09-802-077-58	Sequence 58, Appl
15	17	100.0	17	9	1	US-08-480-547A-2	Sequence 2, Appli
16	17	100.0	17	9	2	US-08-250-847B-2	Sequence 2, Appli
17	17	100.0	17	9	2	US-08-463-949A-2	Sequence 2, Appli
18	17	100.0	17	9	3	US-08-396-385-12	Sequence 12, Appli
19	17	100.0	17	9	3	US-08-464-410A-2	Sequence 2, Appli
20	17	100.0	17	9	3	US-08-159-339A-151	Sequence 151, App
21	17	100.0	17	9	3	US-08-159-339A-164	Sequence 164, App
22	17	100.0	17	9	3	US-08-159-339A-165	Sequence 165, App
23	17	100.0	17	9	3	US-08-159-339A-166	Sequence 166, App
24	17	100.0	17	9	3	US-08-159-339A-167	Sequence 167, App
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27	17	100.0	17	9	3	US-08-159-339A-170	Sequence 170, App
28	17	100.0	17	9	3	US-08-159-339A-171	Sequence 171, App
29	17	100.0	17	9	3	US-09-287-221-12	Sequence 12, Appl
30	17	100.0	17	9	3	US-09-056-461-8	Sequence 8, Appli
31	17	100.0	17	9	5	PCT-US94-06066-2	Sequence 2, Appli
32	17	100.0	17	12	1	US-08-036-555B-164	Sequence 164, App
33	17	100.0	17	12	1	US-08-469-569-164	Sequence 164, App
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35	17	100.0	17	12	2	US-08-466-526A-164	Sequence 164, App
36	17	100.0	17	12	2	US-08-413-490-61	Sequence 61, Appl
37	17	100.0	17	12	2	US-08-734-591A-164	Sequence 164, App
38	17	100.0	17	12	2	US-08-469-660-164	Sequence 164, App
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40	17	100.0	17	12	3	US-08-470-335-164	Sequence 164, App
41	17	100.0	17	12	3	US-08-735-021-164	Sequence 164, App
42	17	100.0	17	12	3	US-08-734-664A-164	Sequence 164, App
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46	17	100.0	17	12	4	US-09-553-042-61	Sequence 61, Appl
47	17	100.0	17	12	5	PCT-US94-05083C-160	Sequence 160, App
48	17	100.0	17	12	5	US-US95-06846A-164	Sequence 164, App
49	17	100.0	17	12	5	PCT-US95-13037-61	Sequence 61, Appl
50	17	100.0	17	13	1	US-08-191-866D-18	Sequence 18, Appl
51	17	100.0	17	13	3	US-08-185-949B-18	Sequence 18, Appl
52	17	100.0	17	13	4	US-09-708-906-17	Sequence 17, Appl
53	17	100.0	17	13	4	US-09-708-906-19	Sequence 19, Appl
54	17	100.0	17	14	3	US-08-232-453A-10	Sequence 10, Appl
55	17	100.0	17	14	4	US-08-232-453A-26	Sequence 26, Appl
56	17	100.0	17	15	3	US-09-009-265-26	Sequence 26, Appl
57	17	100.0	17	15	4	US-08-009-265-28	Sequence 28, Appl
58	17	100.0	17	15	1	US-08-294-434-7	Sequence 7, Appli
59	17	100.0	17	15	1	US-08-45-166-7	Sequence 7, Appli
60	17	100.0	17	15	1	US-08-112-208C-23	Sequence 23, Appl
61	17	100.0	17	15	1	US-08-248-819A-25	Sequence 25, Appl
62	17	100.0	17	15	2	US-08-337-646A-43	Sequence 43, Appl
63	17	100.0	17	15	2	US-08-856-531-23	Sequence 23, Appl
64	17	100.0	17	15	2	US-08-856-034-23	Sequence 23, Appl
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69	17	100.0	17	15	4	US-09-073-010-84	Sequence 84, Appl
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71	17	100.0	17	15	5	PCT-US93-06591-7	Sequence 7, Appli
72	17	100.0	17	16	5	US-08-975-040-11	Sequence 11, Appl
73	17	100.0	17	16	2	US-09-252-556B-57	Sequence 57, Appl
74	17	100.0	17	17	2	US-09-115-209-14	Sequence 14, Appl
75	17	100.0	17	18	1	US-07-913-107-3	Sequence 3, Appli
76	17	100.0	17	18	1	US-08-459-201-3	Sequence 3, Appli
77	17	100.0	17	18	1	US-08-281-248-3	Sequence 3, Appli
78	17	100.0	17	18	2	US-08-664-449-2	Sequence 2, Appli
79	17	100.0	17	18	2	US-08-480-190-27	Sequence 27, Appl
80	17	100.0	17	18	2	US-08-488-379-27	Sequence 27, Appl
81	17	100.0	17	18	2	US-08-818-253-56	Sequence 56, Appl
82	17	100.0	17	18	2	US-08-818-253-61	Sequence 61, Appl
83	17	100.0	17	18	3	US-08-105-454-6	Sequence 6, Appli
84	17	100.0	17	18	3	US-08-818-252-56	Sequence 56, Appl
85	17	100.0	17	18	4	US-08-475-399A-27	Sequence 27, Appl
86	17	100.0	17	18	4	US-08-077-255A-27	Sequence 27, Appl
87	17	100.0	17	18	5	PCT-US93-06421-2	Sequence 2, Appli
88	17	100.0	17	18	5	PCT-US93-07545-27	Sequence 27, Appl
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ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: White, David
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
; TITLE OF INVENTION: Phophodiesterase
; FILE REFERENCE: 5800-28
; CURRENT APPLICATION NUMBER: US/09/330,970
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: 09/277,423
; EARLIER FILING DATE: 1999-03-26
; SOFTWARE: FastSEQ for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-330-970-24

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Best Local Similarity   80.0%; Pred. No. 3.8e+05;
Matches   4; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

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Db   2 LLAAA 6

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; Sequence 38, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: White, David
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide

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Pred. No. is the number of results predicted by chance to have a
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106	100.0	17	26	9	US-09-864-761-33915	Sequence 33915, A
107	100.0	17	26	14	US-10-128-711-115	Sequence 115, App
108	100.0	17	27	10	US-10-915-914B-25	Sequence 25, Appl
109	100.0	17	27	14	US-10-144-549-11	Sequence 11, Appl
110	100.0	17	27	15	US-10-352-839-14	Sequence 14, Appl
111	100.0	17	27	15	US-10-269-711-52	Sequence 52, Appl
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113	100.0	17	27	15	US-10-269-711-55	Sequence 55, Appl
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115	100.0	17	27	16	US-10-684-109-63	Sequence 63, Appl
116	100.0	17	27	16	US-10-684-109-65	Sequence 65, Appl
117	100.0	17	28	16	US-10-684-109-66	Sequence 66, Appl
118	100.0	17	28	10	US-09-070-630-9	Sequence 9, Appli
119	100.0	17	28	14	US-10-351-641-1029	Sequence 1029, Ap
120	100.0	17	28	14	US-10-366-125-23	Sequence 23, Appl
121	100.0	17	29	14	US-10-120-604-14	Sequence 14, Appl
122	100.0	17	29	14	US-10-120-604-48	Sequence 48, Appl
123	100.0	17	30	10	US-09-912-935-30	Sequence 30, Appl
124	100.0	17	30	10	US-09-397-94A-319	Sequence 319, App
125	100.0	17	30	14	US-10-071-174-21	Sequence 21, Appl
126	100.0	17	30	14	US-10-168-365-30	Sequence 30, Appl
127	100.0	17	30	15	US-10-653-599-319	Sequence 319, App
128	100.0	17	32	14	US-10-023-171-73	Sequence 73, Appl
129	100.0	17	32	14	US-10-037-243-10	Sequence 10, Appl
130	100.0	17	33	14	US-10-091-244A-19	Sequence 19, Appl
131	100.0	17	33	14	US-10-072-809A-12	Sequence 12, Appl
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133	100.0	17	33	15	US-10-424-599-170485	Sequence 170485,
134	100.0	17	33	14	US-10-232-410-5	Sequence 5, Appli
135	100.0	17	33	16	US-10-751-380-11	Sequence 11, Appl
136	100.0	17	33	16	US-10-480-172-10	Sequence 10, Appl
137	100.0	17	33	17	US-10-425-115-237036	Sequence 237036,
138	100.0	17	34	10	US-09-962-756-1294	Sequence 1294, Ap
139	100.0	17	34	14	US-10-091-244A-14	Sequence 14, Appl
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141	100.0	17	34	15	US-10-253-493-1294	Sequence 1294, Ap
142	100.0	17	34	16	US-10-437-963-108091	Sequence 108091,
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146	100.0	17	35	14	US-10-083-357-914	Sequence 914, Appl
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159	100.0	17	36	10	US-09-962-756-1314	Sequence 1314, Ap
160	100.0	17	36	10	US-09-962-756-1327	Sequence 1327, Ap
161	100.0	17	36	14	US-10-351-641-751	Sequence 751, App
162	100.0	17	36	14	US-10-253-471-1283	Sequence 1283, Ap
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166	100.0	17	36	14	US-10-253-471-1327	Sequence 1327, Ap
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168	100.0	17	36	15	US-10-253-493-1283	Sequence 1283, Ap
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171	100.0	17	36	15	US-10-253-493-1327	Sequence 1327, Ap
172	100.0	17	36	15	US-10-424-599-154189	Sequence 154189,
173	100.0	17	36	16	US-10-437-963-121562	Sequence 121562,
174	100.0	17	36	16	US-10-767-701-49121	Sequence 49121, A
175	100.0	17	36	16	US-10-425-115-305289	Sequence 305289,
176	100.0	17	37	10	US-09-892-877-366	Sequence 366, App
177	100.0	17	37	10	US-09-948-783-370	Sequence 370, App
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179	100.0	17	37	17	US-10-425-115-197006	Sequence 197006,
180	100.0	17	38	9	US-09-925-442-36	Sequence 36, Appl
181	100.0	17	38	16	US-10-437-963-166299	Sequence 166299,
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183	100.0	17	38	17	US-10-425-115-236977	Sequence 236977,
184	100.0	17	38	17	US-10-425-115-361438	Sequence 361438,
185	100.0	17	39	9	US-09-946-239-13	Sequence 13, Appl
186	100.0	17	39	14	US-10-061-607A-57	Sequence 57, Appl
187	100.0	17	39	14	US-10-351-641-1457	Sequence 1457, Ap
188	100.0	17	39	15	US-10-422-599-245403	Sequence 245403,
189	100.0	17	39	16	US-10-767-701-55789	Sequence 55789, A
190	100.0	17	39	17	US-10-425-115-265434	Sequence 265434,
191	100.0	17	39	17	US-10-425-115-350326	Sequence 350326,
192	100.0	17	40	9	US-09-864-761-34563	Sequence 34563, A
193	100.0	17	40	14	US-10-012-542-315	Sequence 315, Appl
194	100.0	17	40	14	US-10-115-123-315	Sequence 315, Appl
195	100.0	17	40	14	US-10-03-243-16	Sequence 16, Appl
196	100.0	17	40	14	US-10-187-496A-26	Sequence 26, Appl
197	100.0	17	40	14	US-10-187-496A-33	Sequence 33, Appl
198	100.0	17	41	8	US-10-424-599-214715	Sequence 214715,
199	100.0	17	41	8	US-08-424-550B-426	Sequence 426, Appl
200	100.0	17	41	10	US-09-774-639-207	Sequence 207, App

ALIGNMENTS

RESULT 1
US-09-211-424-23
; Sequence 23, Application US/09211424A
; Patent No. US20020177231A1
; GENERAL INFORMATION:
; APPLICANT: Staunton et al.
; TITLE OF INVENTION: Leupaxin Materials and Methods
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/211,424A
; CURRENT FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 23
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: modified human
; OTHER INFORMATION: sequence
US-09-211-424-23

Query Match   100.0%; Score 17; DB 9; Length 6;
Best Local Similarity   80.0%; Pred. No. 1.4e+06;
Matches   4; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 XLAAA 5
              :|||
Db   1 NLAAA 5

holly-13.rpr

```
OM protein - protein search, using sw model

         Copyright   GenCore version 5.1.6
                     (c) 1993 - 2004 Compugen Ltd.

Run on:    November 29, 2004, 07:59:16 ; Search time 16 Seconds
                                (without alignments)
                                30.068 Million cell updates/sec

Title:          HOLLY-13
Perfect score:  17
Sequence:       1 xlaaa 5

Scoring table:  BLOSUM62DX
                Gapop 10.0 , Gapext 0.5

Searched:       283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:    283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :      PIR_79:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	% Match	Query Length	DB	Length	ID	Description
1	17	100.0	17	9	2	A43848	cell surface adhes
2	17	100.0	17	13	2	A38929	glutathione peroxi
3	17	100.0	17	22	2	I59594	monoamine oxidase
4	17	100.0	17	23	2	B37843	vrg 18 protein - B
5	17	100.0	17	26	2	A24735	glutathione transf
6	17	100.0	17	28	2	S21278	glutathione transf
7	17	100.0	17	29	2	C54037	splicing regulator
8	17	100.0	17	30	2	I55427	aspartate transami
9	17	100.0	17	30	2	S13609	glucooligosacchari
10	17	100.0	17	33	1	FDFI5G	antifreeze protein
11	17	100.0	17	33	2	A05162	antifreeze protein
12	17	100.0	17	33	2	PC7035	reversion inducing
13	17	100.0	17	36	2	S73127	hypothetical prote
14	17	100.0	17	36	2	D82482	hypothetical prote
15	17	100.0	17	37	2	C84210	hypothetical prote
16	17	100.0	17	38	2	G81904	antifreeze protein
17	17	100.0	17	40	1	FDFI8G	antifreeze protein
18	17	100.0	17	40	2	A69677	phosphatase (RapC)
19	17	100.0	17	41	2	T16051	hypothetical prote
20	17	100.0	17	41	2	C87484	hypothetical prote
21	17	100.0	17	42	2	S29098	glutathione transf
22	17	100.0	17	43	2	S24180	histone H1.a, test
23	17	100.0	17	43	2	H81142	hypothetical prote
24	17	100.0	17	44	2	T03953	hypothetical prote
25	17	100.0	17	45	2	A05163	antifreeze protein
26	17	100.0	17	45	2	T35464	hypothetical prote
27	17	100.0	17	46	2	AI0624	probable DNA inver
28	17	100.0	17	47	2	A56778	recombination prot
29	17	100.0	17	47	2	AB2489	hypothetical prote
30	17	100.0	17	48	2	S05562	bacteriochlorophyl
31	17	100.0	17	48	2	S05561	bacteriochlorophyl
32	17	100.0	17	48	2	S56664	photosystem II pro
33	17	100.0	17	48	2	A46232	basic helix-loop-h
34	17	100.0	17	48	2	S59076	hypothetical prote
35	17	100.0	17	49	2	S71313	glutathione transf
36	17	100.0	17	49	2	PX0029	protein C inhibito
37	17	100.0	17	50	2	T04338	probable regulator
38	17	100.0	17	51	1	LBRFBS	light-harvesting p
39	17	100.0	17	51	2	S17990	ribosomal protein
40	17	100.0	17	51	2	A26645	light-harvesting p
41	17	100.0	17	51	2	A91003	hypothetical prote
42	17	100.0	17	51	2	AE3604	protein ybgt [impo
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44	17	100.0	17	53	2	PC4101	iron-sulfur protei
45	17	100.0	17	54	2	A46292	zeaxanthin glucosy
46	17	100.0	17	57	2	G84072	hypothetical prote
47	17	100.0	17	59	2	S71066	ribosomal protein
48	17	100.0	17	59	2	F70768	probable PE protei
49	17	100.0	17	60	2	S01652	bacteriochlorophyl
50	17	100.0	17	60	2	T37058	hypothetical prote
51	17	100.0	17	60	2	A40856	organizer-specific
52	17	100.0	17	60	2	A60092	homeotic protein x
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54	17	100.0	17	61	2	F83624	hypothetical prote
55	17	100.0	17	62	2	G91180	hypothetical prote
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57	17	100.0	17	62	2	S47757	hypothetical prote
58	17	100.0	17	63	2	E82775	hypothetical prote
59	17	100.0	17	63	2	B95853	hypothetical prote
60	17	100.0	17	63	2	AI2167	hypothetical prote
61	17	100.0	17	64	2	I40237	hypothetical prote
62	17	100.0	17	64	2	D95331	conserved hypothet
63	17	100.0	17	64	2	AB2271	periplasmic mercur
64	17	100.0	17	65	2	G95061	bacteriocin BlpI [
65	17	100.0	17	65	2	S35024	hypothetical prote
66	17	100.0	17	65	2	AB3381	heavy metal bindin
67	17	100.0	17	66	2	F84205	hypothetical prote
68	17	100.0	17	67	2	S10555	glutathione transf
69	17	100.0	17	67	2	AH0984	conserved hypothet
70	17	100.0	17	67	2	AI1903	hypothetical prote
71	17	100.0	17	68	1	JQBPL	head-to-tail joini
72	17	100.0	17	68	2	G90832	head-to-tail joini
73	17	100.0	17	68	2	B90901	probable head-to-t
74	17	100.0	17	68	2	T44154	hypothetical prote
75	17	100.0	17	68	2	T36853	hypothetical prote
76	17	100.0	17	68	2	E82779	hypothetical prote
77	17	100.0	17	69	2	D49786	lactococcin A1 pre
78	17	100.0	17	69	2	B83632	hypothetical prote
79	17	100.0	17	70	2	I39786	H+-transporting tw
80	17	100.0	17	71	2	I50439	hypothetical prote
81	17	100.0	17	71	2	I50439	vitellogenin III -
82	17	100.0	17	72	2	T08482	plasmid maintenanc
83	17	100.0	17	72	1	LWHWA3	H+-transporting tw
84	17	100.0	17	72	2	T35384	hypothetical prote
85	17	100.0	17	72	2	AE3444	hypothetical prote
86	17	100.0	17	72	2	AD2890	hypothetical prote
87	17	100.0	17	73	2	H97665	histone H1.4 - rab
88	17	100.0	17	73	2	A02579	glucan endo-1,3-be
89	17	100.0	17	73	2	S36020	leghemoglobin l -
90	17	100.0	17	73	2	T10809	hypothetical prote
91	17	100.0	17	73	2	E84279	hypothetical prote
92	17	100.0	17	74	2	B70542	ccg-6 protein [imp
93	17	100.0	17	75	2	T47211	hypothetical prote
94	17	100.0	17	75	2	S70178	glutathione transf
95	17	100.0	17	75	2	F75345	hypothetical prote
96	17	100.0	17	76	2	T45361	hypothetical prote
97	17	100.0	17	76	2	AH0740	DNA-directed DNA p
98	17	100.0	17	76	2	H90947	DNA polymerase III
99	17	100.0	17	76	2	B87584	transcription regu
100	17	100.0	17	76	2	T42309	DNA polymerase III
101	17	100.0	17	76	2	D85796	DNA-directed DNA p
102	17	100.0	17	77	2	S34951	somatotropin precu
					2	PC1017	

No.	%	Len	N	Accession	Description
103	100.0	17	2	S61887	hypothetical prote
104	100.0	17	2	S47941	VMA21 protein - ye
105	100.0	17	2	T09040	hypothetical prote
106	100.0	17	2	A71373	hypothetical prote
107	100.0	17	2	E97064	hypothetical prote
108	100.0	17	2	AE3271	hypothetical membr
109	100.0	17	2	S61446	cellulase (EC 3.2.
110	100.0	17	2	AB3643	hypothetical cytos
111	100.0	17	2	AE3369	hypothetical prote
112	100.0	17	2	AI3344	protein translocas
113	100.0	17	2	S34219	acclimation protei
114	100.0	17	1	LWYCA	H+-transporting tw
115	100.0	17	2	C31090	H+-transporting tw
116	100.0	17	2	AI1807	ATP synthase chain
117	100.0	17	2	G87600	hypothetical prote
118	100.0	17	2	F75409	hypothetical prote
119	100.0	17	2	S20031	hypothetical prote
120	100.0	17	2	B70966	hypothetical prote
121	100.0	17	2	T10320	hypothetical prote
122	100.0	17	2	B95401	hypothetical prote
123	100.0	17	2	S36961	H+-transporting tw
124	100.0	17	2	E70972	probable enoyl-coA
125	100.0	17	2	A47482	pilin-like coloniz
126	100.0	17	2	A97840	hypothetical prote
127	100.0	17	2	B95846	hypothetical prote
128	100.0	17	2	T34904	hypothetical prote
129	100.0	17	2	C95402	hypothetical prote
130	100.0	17	1	QQEC7	hypothetical prote
131	100.0	17	2	G70787	hypothetical prote
132	100.0	17	2	T04475	probable acclimati
133	100.0	17	1	IHTFER	high potential iro
134	100.0	17	2	S48010	Ip5 protein - phag
135	100.0	17	2	G70824	hypothetical prote
136	100.0	17	2	D69268	hypothetical prote
137	100.0	17	2	AC3416	hypothetical Cytos
138	100.0	17	2	AG2402	photosystem I chai
139	100.0	17	2	B96709	hypothetical prote
140	100.0	17	2	S23992	trbE protein - Esc
141	100.0	17	2	AC3459	hypothetical prote
142	100.0	17	2	T29724	hypothetical prote
143	100.0	17	2	AC2723	hypothetical prote
144	100.0	17	2	S25078	acyl carrier prote
145	100.0	17	2	S16161	BLT14 protein - ba
146	100.0	17	2	I68553	cell surface glyco
147	100.0	17	2	S24178	histone H1.d, hepa
148	100.0	17	2	A81013	sugar transport PT
149	100.0	17	2	C84242	hypothetical prote
150	100.0	17	2	T45015	penicillin-binding
151	100.0	17	2	S31949	hypothetical prote
152	100.0	17	2	S56690	hypothetical prote
153	100.0	17	2	A53238	phenomycin - Strep
154	100.0	17	2	AI2287	hypothetical prote
155	100.0	17	2	F82976	probable DNA-bindi
156	100.0	17	2	E81777	probable periplasm
157	100.0	17	1	S09524	mercuric resistanc
158	100.0	17	1	RGEBHD	mercuric resistanc
159	100.0	17	2	T08131	oleosin-like prote
160	100.0	17	2	T45346	hypothetical prote
161	100.0	17	2	D70780	hypothetical prote
162	100.0	17	1	RIPGS	somatostatin I pre
163	100.0	17	2	T08129	oleosin-like prote
164	100.0	17	2	B69150	conserved hypothet
165	100.0	17	2	H84264	conserved hypothet
166	100.0	17	2	S39089	cell wall mannopro
167	100.0	17	2	D87257	conserved hypothet
168	100.0	17	2	B36942	fptB protein - Pse
169	100.0	17	2	C82440	hypothetical prote
170	100.0	17	2	AF3485	hypothetical prote
171	100.0	17	1	COSJS	1G2 protein - brac
172	100.0	17	2	E84281	hypothetical prote
173	100.0	17	2	F31844	spdA protein - Str
174	100.0	17	2	T03285	anther-specific pr
175	100.0	17	2	C98239	hypothetical prote

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176	100.0	17	95	2	S31081	seed allergen RAG1
177	100.0	17	95	2	H86966	hypothetical prote
178	100.0	17	95	2	D83325	hypothetical prote
179	100.0	17	95	2	A70803	early secretory an
180	100.0	17	95	2	B45519	variant surface gl
181	100.0	17	96	2	AB0853	hypothetical prote
182	100.0	17	96	2	T17845	hypothetical prote
183	100.0	17	96	2	T35372	probable membrane
184	100.0	17	96	2	T28327	ORF MSV166 hypothe
185	100.0	17	97	2	AB2005	30S ribosomal prot
186	100.0	17	97	2	S76406	hypothetical prote
187	100.0	17	97	2	T28947	hypothetical prote
188	100.0	17	97	2	F97780	hypothetical prote
189	100.0	17	98	2	F70511	probable PE protei
190	100.0	17	98	2	B70568	probable PE protei
191	100.0	17	98	2	F83404	hypothetical prote
192	100.0	17	98	2	T28629	Y4cB protein - Rhi
193	100.0	17	98	2	D75519	hypothetical prote
194	100.0	17	98	2	AI2262	hypothetical prote
195	100.0	17	99	1	S40865	C4-dicarboxylate t
196	100.0	17	99	2	G86081	hypothetical prote
197	100.0	17	99	2	G91234	hypothetical prote
198	100.0	17	99	2	A70608	probable PE protei
199	100.0	17	99	2	A70930	probable PE Protei
200	100.0	17	99	2	D70582	probable PE protei

ALIGNMENTS

RESULT 1

A43848

cell surface adhesin for heparan sulfate, 66K - Staphylococcus aureus (fragment)
C;Species: Staphylococcus aureus
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A43848
R;Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.
Infect. Immun. 60, 899-906, 1992
A;Title: Binding of heparan sulfate to Staphylococcus aureus.
A;Reference number: A43848; MUID:92176005; PMID:1541563
A;Accession: A43848
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LIA>
A;Cross-references: UNIPROT:Q9R5M1
A;Note: sequence extracted from NCBI backbone (NCBIP:85442)

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Query Match             100.0%;  Score 17;  DB 2;  Length 9;
Best Local Similarity   80.0%;  Pred. No. 2.8e+05;
Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 XLAAA 5
              :||||
Db          5 WLAAA 9
```

RESULT 2

A38929

glutathione peroxidase (EC 1.11.1.9) - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A38929
R;Gettins, P.; Dyal, D.; Crews, B.
Arch. Biochem. Biophys. 294, 511-518, 1992
A;Title: Selenium-dependent glutathione peroxidases from ovine and bovine erythrocytes
A;Reference number: S21712; MUID:92231574; PMID:1567207
A;Accession: A38929
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <GET>
A;Cross-references: UNIPROT:Q7M355
C;Superfamily: glutathione peroxidase
C;Keywords: oxidoreductase

OM protein - protein search, using sw model

```
                GenCore version 5.1.6
        Copyright  (c) 1993 - 2004  Compugen Ltd.

Run on:    November 29, 2004, 07:58:41 ; Search time 62 Seconds
                              (without alignments)
                              46.401 Million cell updates/sec

Title:          HOLLY-13
Perfect score:  17
Sequence:       1 xlaaa 5

Scoring table:  BLOSUM62DX
                Gapop 10.0 , Gapext 0.5

Searched:       1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters:   1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :  UniProt_02:*
            1: uniprot_sprot:*
            2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result NO.	Score	% Match	Query Match	Length	DB	ID	Description
1	17	100.0	17	9	2	Q9R5M1	staphylococc
2	17	100.0	17	10	2	Q94II9	zea mays (m
3	17	100.0	17	13	2	Q7M355	ovis aries
4	17	100.0	17	15	2	Q9FYY6	gossypium h
5	17	100.0	17	16	2	Q9JHM3	rattus norv
6	17	100.0	17	17	2	Q7JMY3	leishmania
7	17	100.0	17	19	2	Q7YK33	chloroleuco
8	17	100.0	17	21	2	Q9UCJ6	homo sapien
9	17	100.0	17	22	2	AOFA_MOUSE	mus musculu
10	17	100.0	17	22	2	Q7L8R0	homo sapien
11	17	100.0	17	22	2	CAA22266	homo sapi
12	17	100.0	17	23	2	Q8MFI3	crepidomane
13	17	100.0	17	23	2	Q8MFI5	sphaerocion
14	17	100.0	17	23	2	Q8MFI7	hymenophyll
15	17	100.0	17	23	2	Q8MFI9	hymenophyll
16	17	100.0	17	23	2	Q8MFJ1	hymenophyll
17	17	100.0	17	23	2	Q8MEJ3	hymenophyll
18	17	100.0	17	23	2	Q8MFJ5	hymenophyll
19	17	100.0	17	23	2	Q8MFJ7	hymenophyll
20	17	100.0	17	23	2	Q8MRJ9	hymenophyll
21	17	100.0	17	23	2	Q8MFK1	hymenophyll
22	17	100.0	17	23	2	Q8MFK3	hymenophyll
23	17	100.0	17	23	2	Q8MFK5	hymenophyll
24	17	100.0	17	23	2	Q04274	bordetella
25	17	100.0	17	23	2	Q84F40	streptomyce
26	17	100.0	17	24	2	Q8R2H8	mus musculu
27	17	100.0	17	27	1	PSBY_FUCVE	fucus vesic
28	17	100.0	17	27	2	Q6V100	mus spretus
29	17	100.0	17	27	2	Q80WY7	rattus sp.
30	17	100.0	17	27	2	AAQ55837	mus spret
31	17	100.0	17	28	2	Q8IZL0	homo sapien
32	17	100.0	17	28	2	Q71KP5	spirogyra m
33	17	100.0	17	28	2	Q79CG0	neisseria g
34	17	100.0	17	28	2	Q7VEL4	mycobacteri
35	17	100.0	17	28	2	Q6MX19	mycobacteri
36	17	100.0	17	28	2	Q9QVC9	rattus sp.
37	17	100.0	17	28	2	AAB63319	neisseria
38	17	100.0	17	28	2	AAQ05912	spirogyra
39	17	100.0	17	28	2	CAE55539	mycobacte
40	17	100.0	17	29	1	PETI1_CYAME	cyanidiosch
41	17	100.0	17	29	2	Q9JLQ6	rattus norv
42	17	100.0	17	29	2	AAF63713	homo sapi
43	17	100.0	17	30	2	Q9URB6	acremonium
44	17	100.0	17	30	2	Q9BWZ3	homo sapien
45	17	100.0	17	30	2	Q6LBU2	triticum ae
46	17	100.0	17	30	2	CAA31327	triticum
47	17	100.0	17	31	1	DIUX_DIPPU	diploptera
48	17	100.0	17	31	2	Q9FUQ2	zea mays (s
49	17	100.0	17	31	2	Q80RG7	newcastle d
50	17	100.0	17	32	2	Q96RX4	homo sapien
51	17	100.0	17	32	2	Q9MVP0	arabidopsis
52	17	100.0	17	32	2	Q9G264	polygonum c
53	17	100.0	17	32	2	Q9G265	polygonum c
54	17	100.0	17	32	2	Q9G266	polygonum c
55	17	100.0	17	32	2	Q9GFQ7	polygonum w
56	17	100.0	17	32	2	Q9GFR3	polygonum s
57	17	100.0	17	32	2	Q9FE80	zea diplope
58	17	100.0	17	32	2	Q9FE81	zea mays (s
59	17	100.0	17	32	2	Q9FE82	zea mays (s
60	17	100.0	17	32	2	Q9FUP8	zea luxuria
61	17	100.0	17	32	2	Q9FUP9	zea luxuria
62	17	100.0	17	32	2	Q9FUQ0	zea luxuria
63	17	100.0	17	32	2	Q9FUQ1	zea mays (s
64	17	100.0	17	32	2	Q9FUQ3	zea mays (s
65	17	100.0	17	32	2	Q9FUQ4	zea mays (s
66	17	100.0	17	32	2	Q9FUQ5	zea mays (m
67	17	100.0	17	32	2	Q72F90	desulfovibr
68	17	100.0	17	32	2	AAS94807	desulfovi
69	17	100.0	17	33	1	ANP3_MYOSC	myoxocephal
70	17	100.0	17	33	1	ANP5_MYOAE	myoxocephal
71	17	100.0	17	33	2	Q72ZM7	homo sapien
72	17	100.0	17	34	2	Q6XQJ3	pseudomonas
73	17	100.0	17	34	2	AAP49281	pseudomon
74	17	100.0	17	35	1	PETG_CYACA	cyanidium c
75	17	100.0	17	36	1	PSBY_PORPU	porphyra pu
76	17	100.0	17	36	2	Q7JMV4	anopheles g
77	17	100.0	17	36	2	Q9KMR8	vibrio chol
78	17	100.0	17	37	1	PSBY_GUITH	guillardia
79	17	100.0	17	37	2	Q9HRW1	halobacteri
80	17	100.0	17	37	2	Q8LID9	vibrio angu
81	17	100.0	17	37	2	Q98A46	rhizobium l
82	17	100.0	17	38	2	Q7SHL3	neurospora
83	17	100.0	17	38	2	Q7SI50	neurospora
84	17	100.0	17	38	2	Q939W1	aeromonas s
85	17	100.0	17	38	2	Q9JUE4	neisseria m
86	17	100.0	17	38	2	Q8VIU8	mycobacteri
87	17	100.0	17	40	1	ANP8_MYOAE	myoxocephal
88	17	100.0	17	40	1	PHRC_BACSU	bacillus su
89	17	100.0	17	40	2	Q9TNZ4	rattus norv
90	17	100.0	17	40	2	Q6DL79	bacillus mo
91	17	100.0	17	40	2	Q6DL81	bacillus su
92	17	100.0	17	41	2	Q9TNZ5	rattus norv
93	17	100.0	17	41	2	Q53456	streptomyce
94	17	100.0	17	41	2	Q9A730	caulobacter
95	17	100.0	17	42	2	Q7X5B5	synechococc
96	17	100.0	17	42	2	Q7M0F6	mesocricetu
97	17	100.0	17	42	2	Q69019	human herpe
98	17	100.0	17	42	2	Q9DF18	myoxocephal
99	17	100.0	17	43	2	Q7LJQ2	fusarium ps
100	17	100.0	17	43	2	Q7LJT0	fusarium cu
101	17	100.0	17	43	2	Q7LJT5	fusarium lu
102	17	100.0	17	43	2	Q7LP62	gibberella
103	17	100.0	17	43	2	Q8NJE8	fusarium ce
104	17	100.0	17	43	2	Q9C1A7	fusarium ce

No.	ID	Score	DB	%	Q	S	Accession	Description
105	Q9C1B4	43	2	100.0	17	17	Q9C1B4	fusarium sp
106	Q6EAS2	43	2	100.0	17	17	Q6EAS2	equus caball
107	Q9TN26	43	2	100.0	17	17	Q9TN26	rattus norv
108	Q9L7I0	43	2	100.0	17	17	Q9L7I0	synechococc
109	Q9JZS3	43	2	100.0	17	17	Q9JZS3	neisseria m
110	Q8XW38	43	2	100.0	17	17	Q8XW38	ralstonia s
111	Q6EWA2	43	2	100.0	17	17	Q6EWA2	human calci
112	Q95562	44	2	100.0	17	17	Q95562	rattus norv
113	O24577	44	2	100.0	17	17	O24577	zea mays (m
114	Q9L7E4	44	2	100.0	17	17	Q9L7E4	synechococc
115	Q7UPL2	44	2	100.0	17	17	Q7UPL2	rhodopirell
116	Q8EZ88	44	2	100.0	17	17	Q8EZ88	leptospira
117	P04368	44	2	100.0	17	17	P04368	myxocephal
118	ANP8_MYOSC	45	1	100.0	17	17	ANP8_MYOSC	mycobacteri
119	Q7I6R4	45	2	100.0	17	17	Q7I6R4	proteus mir
120	Q6X937	45	2	100.0	17	17	Q6X937	paracoccus
121	Q7B303	45	2	100.0	17	17	Q7B303	gallus gall
122	Q6LEL2	45	2	100.0	17	17	Q6LEL2	mycobacte
123	AAQ12088	45	2	100.0	17	17	AAQ12088	gallus ga
124	AAD10202	45	2	100.0	17	17	AAD10202	proteus m
125	AAP76377	46	2	100.0	17	17	AAP76377	mycoplasma
126	Q9ZID2	46	2	100.0	17	17	Q9ZID2	porphyromon
127	Q7MUH0	46	2	100.0	17	17	Q7MUH0	brucella su
128	Q8FUU7	46	2	100.0	17	17	Q8FUU7	salmonella
129	Q8Z7T3	47	2	100.0	17	17	Q8Z7T3	pseudomonas
130	RECA_PSEST	47	1	100.0	17	17	RECA_PSEST	giardia lam
131	Q7QXV1	47	2	100.0	17	17	Q7QXV1	zea mays (m
132	Q41781	47	2	100.0	17	17	Q41781	prochloroco
133	Q9X1F9	47	2	100.0	17	17	Q9X1F9	anabaena sp
134	Q8YL45	47	2	100.0	17	17	Q8YL45	coturnix co
135	Q90329	47	2	100.0	17	17	Q90329	gallus gall
136	Q90774	48	2	100.0	17	17	Q90774	chlorobium
137	CSMA_CHLLT	48	1	100.0	17	17	CSMA_CHLLT	prosthecoch
138	CSMA_PROAE	48	1	100.0	17	17	CSMA_PROAE	pinus pinas
139	RBL_PINPS	48	1	100.0	17	17	RBL_PINPS	anopheles g
140	Q8WR24	48	2	100.0	17	17	Q8WR24	zea mays (m
141	Q05461	48	2	100.0	17	17	Q05461	streptomyce
142	Q02801	48	2	100.0	17	17	Q02801	cellulomona
143	Q46040	48	2	100.0	17	17	Q46040	pseudomonas
144	Q88JK5	48	2	100.0	17	17	Q88JK5	yersinia pe
145	Q8CKM0	48	2	100.0	17	17	Q8CKM0	brucella su
146	Q8G2K2	48	2	100.0	17	17	Q8G2K2	tetraodon n
147	Q9TBB5	49	2	100.0	17	17	Q9TBB5	neurospora
148	Q7S4A4	49	2	100.0	17	17	Q7S4A4	drosophila
149	Q9SN2	49	2	100.0	17	17	Q9SN2	xanthomonas
150	Q7WYV8	49	2	100.0	17	17	Q7WYV8	rhizobium m
151	Q92R21	49	2	100.0	17	17	Q92R21	mycobacteri
152	Q8VJI0	49	2	100.0	17	17	Q8VJI0	mycobacteri
153	Q8VJQ9	49	2	100.0	17	17	Q8VJQ9	mus musculu
154	Q7M0B9	50	2	100.0	17	17	Q7M0B9	rhodobacter
155	LHB2_RHOSH	50	1	100.0	17	17	LHB2_RHOSH	anopheles g
156	Q7PFV7	50	2	100.0	17	17	Q7PFV7	zea mays (m
157	O04724	50	2	100.0	17	17	O04724	triticum ae
158	Q9SM32	50	2	100.0	17	17	Q9SM32	synechococc
159	Q917F4	50	2	100.0	17	17	Q917F4	bordetella
160	Q7VZM4	50	2	100.0	17	17	Q7VZM4	bordetella
161	Q7WM35	50	2	100.0	17	17	Q7WM35	mycobacteri
162	Q8VKL5	50	2	100.0	17	17	Q8VKL5	mamestra co
163	Q71AA5	50	2	100.0	17	17	Q71AA5	mamestra co
164	Q8LC7	51	2	100.0	17	17	Q8LC7	mamestra
165	AAQ11126	51	2	100.0	17	17	AAQ11126	pyrobaculum
166	RL39_PYRAE	51	1	100.0	17	17	RL39_PYRAE	homo sapien
167	Q8TBL2	51	2	100.0	17	17	Q8TBL2	oryza sativ
168	Q8GVM9	51	2	100.0	17	17	Q8GVM9	arabidopsis
169	Q8LCJ2	51	2	100.0	17	17	Q8LCJ2	oryza sativ
170	Q9FP56	51	2	100.0	17	17	Q9FP56	arabidopsis
171	Q94LB1	51	2	100.0	17	17	Q94LB1	vibrio fisc
172	Q9AJQ9	51	2	100.0	17	17	Q9AJQ9	chromobacte
173	Q7NYK6	51	2	100.0	17	17	Q7NYK6	mycobacteri
174	Q7W8H3	51	2	100.0	17	17	Q7W8H3	mycobacteri
175	Q8VKP0	51	2	100.0	17	17	Q8VKP0	escherichia
176	Q8X2Z0	51	2	100.0	17	17	Q8X2Z0	brucella me
177	Q8YBX8	51	2	100.0	17	17	Q80OJ8	plecoglossu
178	Q8AWH5	51	2	100.0	17	17	Q8AWH5	pseudopleur
179	Q9I821	51	2	100.0	17	17	Q9I821	oncorhynchu
180	Q9PSE5	51	2	100.0	17	17	Q9PSE5	oncorhynchu
181	Q9PSE6	51	2	100.0	17	17	Q9PSE6	carassius a
182	Q9PSE7	51	2	100.0	17	17	Q9PSE7	carassius a
183	Q6MIF9	52	2	100.0	17	17	Q6MIF9	homo sapien
184	Q6ZAK4	52	2	100.0	17	17	Q6ZAK4	oryza sativ
185	Q98AH5	52	2	100.0	17	17	Q98AH5	rhizobium l
186	Q8XY97	52	2	100.0	17	17	Q8XY97	ralstonia s
187	Q7M5J7	52	2	100.0	17	17	Q7M5J7	fowl adenov
188	CAE46080	52	2	100.0	17	17	CAE46080	homo sapi
189	BAC99634	53	2	100.0	17	17	BAC99634	oryza sat
190	Q28023	53	2	100.0	17	17	Q28023	bos taurus
191	Q28551	53	2	100.0	17	17	Q28551	ovis aries
192	Q8RZF2	53	2	100.0	17	17	Q8RZF2	oryza sativ
193	Q79F45	53	2	100.0	17	17	Q79F45	rhodobacter
194	Q98EX6	53	2	100.0	17	17	Q98EX6	rhizobium l
195	Q8VJ18	53	2	100.0	17	17	Q8VJ18	mycobacteri
196	Q8X2S0	53	2	100.0	17	17	Q8X2S0	escherichia
197	Q9EP65	53	2	100.0	17	17	Q9EP65	mus musculu
198	O11370	54	2	100.0	17	17	O11370	molluscum c
199	Q853H8	54	2	100.0	17	17	Q853H8	mycobacteri
200	Q9XCY9	54	2	100.0	17	17	Q9XCY9	streptomyce

ALIGNMENTS

RESULT 1
Q9R5M1

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ID   Q9R5M1      PRELIMINARY;   PRT;    9 AA.
AC   Q9R5M1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   66 kDa cell surface adhesin for heparan sulfate (Fragment).
OS   Staphylococcus aureus.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=1280;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92176005; PubMed=1541563;
RA   Liang O.D., Ascencio F., Fransson L.A., Wadstrom T.;
RT   "Binding of heparan sulfate to Staphylococcus aureus.";
RL   Infect. Immun. 60:899-906(1992).
DR   PIR; A43848; A43848.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;   990 MW;  2289DDD7337861B3 CRC64;

Query Match          100.0%;   Score 17;   DB 2;   Length 9;
Best Local Similarity  80.0%;   Pred. No. 1.8e+06;
Matches    4;   Conservative    1;   Mismatches    0;   Indels    0;   Gaps    0;

Qy      1 XLAAA 5
          :||||
Db      5 WLAAA 9
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RESULT 2
Q94II9

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ID   Q94II9      PRELIMINARY;   PRT;   10 AA.
AC   Q94II9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Anthocyanin regulator R-sc protein (Fragment).
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
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